Antibiotic susceptibility and genetic relatedness of Shigella species isolated from food and human stool samples in Qazvin, Iran

Babak Pakbin [1 2], Abdollah Didban [3], Yousef Khazaye Monfared [4], Razzagh Mahmoudi [2], Amir Peymani [2], Mohammad Reza Modabber [2]
Affiliations collapse

- [1]Children Growth Research Center, Research Institute for Prevention of Non-Communicable Diseases, Qazvin University of Medical Sciences, Bahonar Blvd., P.O. Box: 34185-754, Qazvin, Iran.
- [2]Medical Microbiology Research Center, Qazvin University of Medical Sciences, Qazvin, Iran.
- [3]Children Growth Research Center, Research Institute for Prevention of Non-Communicable Diseases, Qazvin University of Medical Sciences, Bahonar Blvd., P.O. Box: 34185-754, Qazvin, Iran. drdidban@yahoo.com.
- [4]M.Sc. of Medical-Biotechnology, Dezful University of Medical Sciences, Dezful, Iran.

Abstract

Objective: The aim of this study was to investigate the genetic relatedness and antimicrobial resistance among Shigella species isolated from food and stool samples. Using cross sectional study method, Shigella spp. were isolated from food and clinical samples using culture-based, biochemical and serological methods. Antimicrobial susceptibility and genetic relatedness among the isolates were evaluated using disk diffusion and RAPD-PCR methods respectively.

Results: The prevalence of Shigella spp. were 4.84 and 7.7% in food and stool samples respectively. All food isolates were Sh. sonnei. 91.42% of the Shigella stool isolates were Sh. sonnei. 62.5% of food isolates were resistant to tetracycline. 46.8, 50 and 65.8% of clinical isolates were resistant to imipenem, amikacin and azithromycin respectively. 50 and 85.7% of the food and clinical isolates respectively were MDR. Dendrogram generated by RAPD-PCR showed that the isolates from food and stool samples were categorized in a same group. Close genetic relatedness between MDR Shigella isolates from food and clinical samples indicate that foods can be considered as one of the main vehicles for transmission of MDR Shigella to human causing acute diseases. Survey of MDR Shigella among food and clinical samples is strongly suggested to be implemented.

Keywords: Antimicrobial susceptibility; Food samples; Genetic relatedness; Shigella species; Stool specimens.